TWIK 2

Input file FthKa020g04.seq; Output File FthKa020g04.tra
Sequence length 3452

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 I   G   A   A   I   F   E   V   L   E   E   P   H   W   K   E   A   K   K   N
ATC GGG GCG GCG ATC TTC GAA GTG CTG GAG GAG CCA CAC TGG AAG GAG GCC AAG AAA AAC
 Y   Y   T   Q   K   L   H   L   L   K   E   F   P   C   L   G   Q   E   G   L
TAC TAC ACA CAG AAG CTG CAT CTG CTC AAG GAG TTC CCG TGC CTG GGT CAG GAG GGC CTG
 D   K   I   L   E   V   V   S   D   A   A   G   Q   G   V   A   I   T   G   N
GAC AAG ATC CTA GAG GTG GTA TCT GAT GCT GCA GGA CAG GGT GTG GCC ATC ACA GGG AAC
 Q   T   F   N   N   W   N   W   P   N   A   M   I   F   A   A   T   V   I   T
CAG ACC TTC AAC AAC TGG AAC TGG CCC AAT GCA ATG ATT TTT GCA GCG ACC GTC ATT ACC
 T   I   G   Y   G   N   V   A   P   K   T   P   A   G   R   L   F   C   V   F
ACC ATT GGA TAT GGC AAT GTG GCT CCC AAG ACC CCC GCC GGT CGC CTC TTC TGT GTT TTC
 Y   G   L   F   G   V   P   L   C   L   T   W   I   S   A   L   G   K   F   F
TAT GGT CTC TTC GGG GTG CCG CTC TGC CTG ACG TGG ATC AGT GCC CTG GGC AAG TTC TTC
 G   G   R   A   K   R   L   G   Q   F   L   T   K   R   G   V   S   L   R   K
GGG GGA CGT GCC AAG AGA CTA GGG CAG TTC CTT ACC AAG AGA GGT GTG AGT CTG CGG AAG
 A   Q   I   T   C   T   V   I   F   I   V   W   G   V   L   V   H   L   V   I
GCG CAG ATC ACG TGC ACA GTC ATC TTC ATC GTG TGG GGC GTC CTA GTC CAC CTG GTG ATC
 P   P   F   V   F   M   V   T   E   G   W   N   Y   I   E   G   L   Y   Y   S
CCA CCC TTC GTA TTC ATG GTG ACT GAG GGG TGG AAC TAC ATC GAG GGC CTC TAC TAC TCC
 F   I   T   I   S   T   I   G   F   G   D   F   V   A   G   V   N   P   S   A
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 N   Y   H   A   L   Y   R   Y   F   V   E   L   W   I   Y   L   G   L   A   W
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 L   S   L   F   V   N   W   K   V   S   M   F   V   E   V   H   K   A   I   K
CTG TCC CTT TTT GTC AAC TGG AAG GTG AGC ATG TTT GTG GAA GTC CAC AAA GCC ATT AAG
 K   R   R   R   R   R   K   E   S   F   E   S   S   P   H   S   R   K   A   L
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 Q   V   K   G   S   T   A   S   K   D   V   N   I   F   S   F   L   S   K   K
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 E   E   T   Y   N   D   L   I   K   Q   I   G   K   K   A   M   K   T   S   G
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 G   G   E   T   G   P   G   P   G   L   G   P   Q   G   G   G   L   P   A   L
GGT GGG GAG ACG GGC CCG GGC CCA GGG CTG GGG CCT CAA GGC GGT GGG CTC CCA GCA CTG
 P   P   S   L   V   P   L   V   V   Y   S   K   N   R   V   P   T   L   E   E
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 V   S   Q   T   L   R   S   K   G   H   V   S   R   S   P   D   E   E   A   V
GTG TCA CAG ACA CTG AGG AGC AAA GGC CAC GTA TCA AGG TCC CCA GAT GAG GAG GCT GTG
 A   R   A   P   E   D   S   S   P   A   P   E   V   F   M   N   Q   L   D   R
GCA CGG GCC CCT GAA GAC AGC TCC CCT GCC CCC GAG GTG TTC ATG AAC CAG CTG GAC CGC
 I   S   E   E   C   E   P   W   D   A   Q   D   Y   H   P   L   I   F   Q   D
ATC AGC GAG GAA TGC GAG CCA TGG GAC GCC CAG GAC TAC CAC CCA CTC ATC TTC CAG GAC
 A   S   I   T   F   V   N   T   E   A   G   L   S   D   E   E   T   S   K   S
GCC AGC ATC ACC TTC GTG AAC ACG GAG GCT GGC CTC TCA GAC GAG GAG ACC TCC AAG TCC
 S   L   E   D   N   L   A   G   E   E   S   P   Q   Q   G   A   E   A   K   A
TCG CTA GAG GAC AAC TTG GCA GGG GAG GAG AGC CCC CAG CAG GGG GCT GAA GCC AAG GCG
```

Fig. 1

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 P   L   N   M   G   E   F   P   S   S   S   E   S   T   F   T   S   T   E   S
CCC CTG AAC ATG GGC GAG TTC CCC TCC TCC TCC GAG TCC ACC TTC ACC AGC ACT GAG TCT
 E   L   S   V   P   Y   E   Q   L   M   N   E   Y   N   K   A   N   S   P   K
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 G   T   *
GGC ACA TGA
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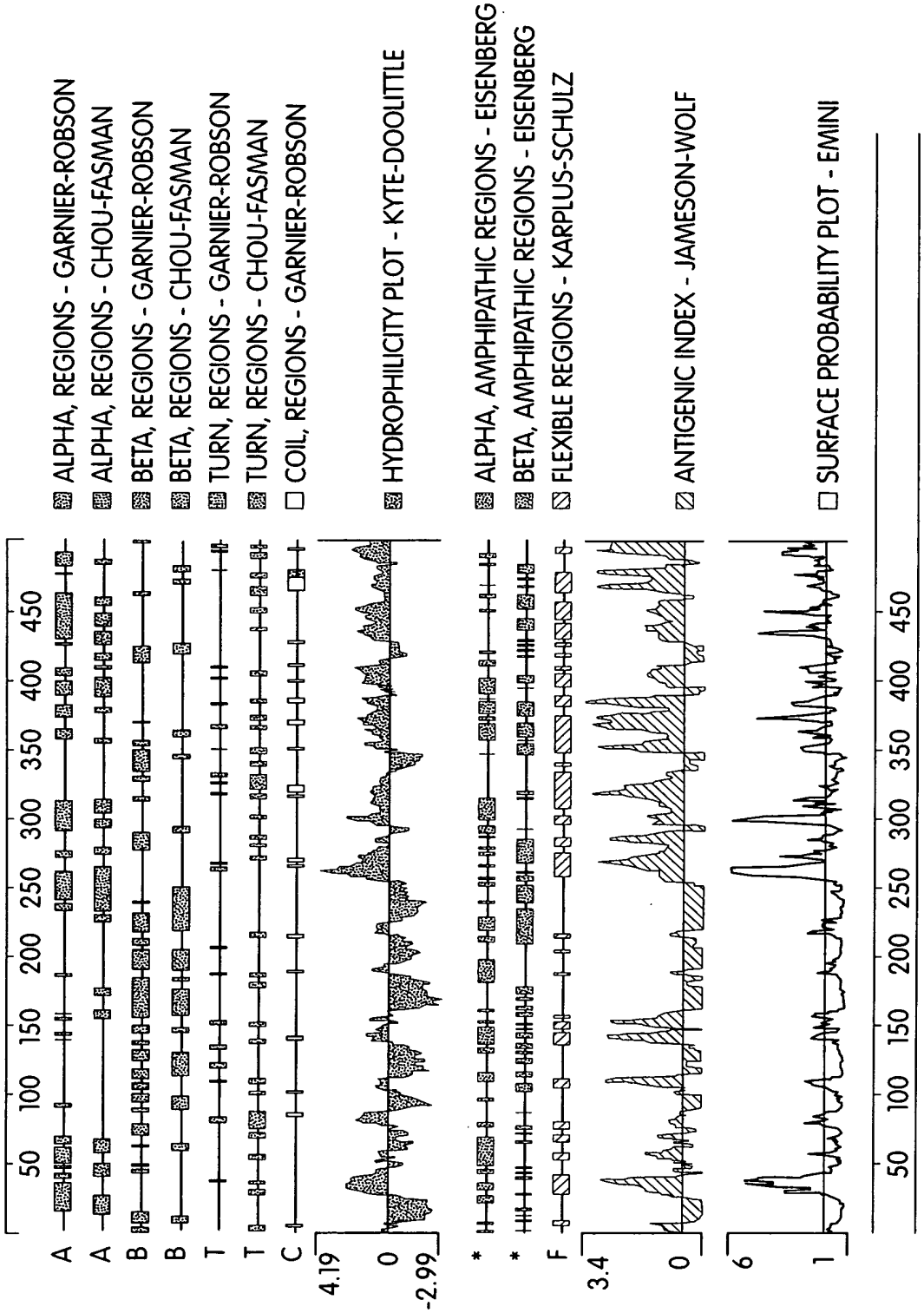
Fig. 1 (continued)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ANTIGENIC INDEX - JAMESON-WOLF
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Fig. 2

Input file Athua133f10.seq; Output File Athua133f10.tra
Sequence length 1575

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 P   E   G   R   V   R   G   C   A   V   P   G   T   V   L   L   L   L   A   Y
CCC GAG GGC AGG GTC CGG GGC TGC GCG GTG CCC GGC ACC GTG CTC CTG CTG CTC GCC TAC
 L   A   Y   L   A   L   G   T   G   V   F   W   T   L   E   G   R   A   A   Q
CTG GCT TAC CTG GCG CTG GGC ACC GGC GTG TTC TGG ACG CTG GAG GGC CGC GCG GCG CAG
 D   S   S   R   S   F   Q   R   D   K   W   E   L   L   Q   N   F   T   C   L
GAC TCC AGC CGC AGC TTC CAG CGC GAC AAG TGG GAG CTG TTG CAG AAC TTC ACG TGT CTG
 D   R   P   A   L   D   S   L   I   R   D   V   V   Q   A   Y   K   N   G   A
GAC CGC CCG GCG CTG GAC TCG CTG ATC CGG GAT GTC GTC CAA GCA TAC AAA AAC GGA GCC
 S   L   L   S   N   T   T   S   M   G   R   W   E   L   V   G   S   F   F   F
AGC CTC CTC AGC AAC ACC ACC AGC ATG GGG CGC TGG GAG CTC GTG GGC TCC TTC TTC TTT
 S   V   S   T   I   T   T   I   G   Y   G   N   L   S   P   N   T   M   A   A
TCT GTG TCC ACC ATC ACC ACC ATT GGC TAT GGC AAC CTG AGC CCC AAC ACG ATG GCT GCC
 R   L   F   C   I   F   F   A   L   V   G   I   P   L   N   L   V   V   L   N
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 R   L   G   H   L   M   Q   Q   G   V   N   H   W   A   S   R   L   G   G   T
CGA CTG GGG CAT CTC ATG CAG CAG GGA GTA AAC CAC TGG GCC AGC AGG CTG GGG GGC ACC
 W   Q   D   P   D   K   A   R   W   L   A   G   S   G   A   L   L   S   G   L
TGG CAG GAT CCT GAC AAG GCG CGG TGG CTG GCG GGC TCT GGC GCC CTC CTC TCG GGC CTC
 L   L   F   L   L   L   P   P   L   L   F   S   H   M   E   G   W   S   Y   T
CTG CTC TTC CTG CTG CTG CCA CCG CTG CTC TTC TCC CAC ATG GAG GGC TGG AGC TAC ACA
 E   G   F   Y   F   A   F   I   T   L   S   T   V   G   F   G   D   Y   V   I
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 G   M   N   P   S   Q   R   Y   P   L   W   Y   K   N   M   V   S   L   W   I
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 L   F   G   M   A   W   L   A   L   I   I   K   L   I   L   S   Q   L   E   T
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 P   G   R   V   C   S   C   C   H   H   S   S   K   E   D   F   K   S   Q   S
CCA GGG AGG GTA TGT TCC TGC TGC CAC CAC AGC TCT AAG GAA GAC TTC AAG TCC CAA AGC
 W   R   Q   G   P   D   R   E   P   E   S   H   S   P   Q   Q   G   C   Y   P
TGG AGA CAG GGA CCT GAC CGG GAG CCA GAG TCC CAC TCC CCA CAG CAA GGA TGC TAT CCA
 E   G   P   M   G   I   I   Q   H   L   E   P   S   A   H   A   A   G   C   G
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 K   D   S   *
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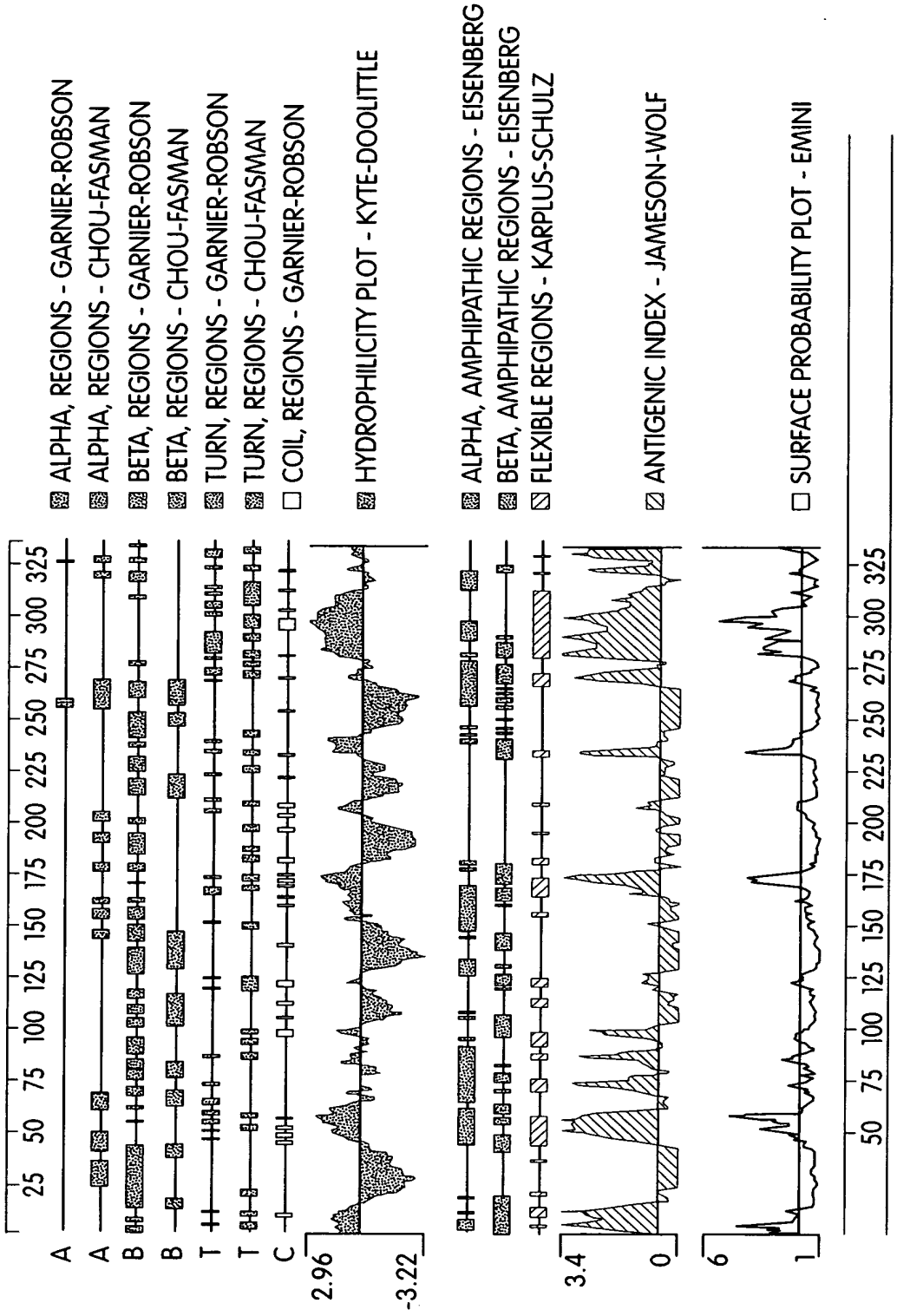
Fig. 3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COIL, REGIONS - GARNIER-ROBSON
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ANTIGENIC INDEX - JAMESON-WOLF
SURFACE PROBABILITY PLOT - EMINI
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A
B
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T
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Fig. 4

TWIK 4

Input file AthTb005e07.seq; Output File AthTb005e07.tra
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 A   R   L   E   G   P   H   E   A   R   L   R   A   E   L   E   T   L   R   A
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 Q   L   L   Q   R   S   P   C   V   A   A   P   A   L   D   A   F   V   E   R
CAG CTG CTT CAG CGC AGC CCG TGT GTG GCT GCC CCC GCC CTG GAC GCC TTC GTG GAG CGA
 V   L   A   A   G   R   L   G   R   V   V   L   A   N   A   S   G   S   A   N
GTG CTG GCG GCC GGA CGG CTG GGG CGG GTC GTG CTT GCT AAC GCT TCG GGG TCC GCC AAC
 A   S   D   P   A   W   D   F   A   S   A   L   F   F   A   S   T   L   I   T
GCC TCG GAC CCC GCC TGG GAC TTC GCC TCT GCT CTC TTC TTC GCC AGC ACG CTG ATC ACC
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ACC GTG GGC TAT GGG TAC ACA ACG CCA CTG ACT GAT GCG GGC AAG GCC TTC TCC ATC GCC
 F   A   L   L   G   V   P   T   T   M   L   L   L   T   A   S   A   Q   R   L
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 R   R   A   A   C   W   H   L   V   A   L   L   G   V   V   V   T   V   C   F
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CTG GTG CCG GCT GTG ATC TTT GCC CAC CTC GAG GAG GCC TGG AGC TTC TTG GAT GCC TTC
 Y   F   C   F   I   S   L   S   T   I   G   L   G   D   Y   V   P   G   E   A
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 P   G   Q   P   Y   R   A   L   Y   K   V   L   V   T   V   Y   L   F   L   G
CCT GGC CAG CCC TAC CGG GCC CTC TAC AAG GTG CTG GTC ACA GTC TAC CTC TTC CTG GGC
 L   V   A   M   V   L   V   L   Q   T   F   R   H   V   S   D   L   H   G   L
CTG GTG GCC ATG GTG CTG GTG CTG CAG ACC TTC CGC CAC GTG TCC GAC CTC CAC GGC CTC
 T   E   L   I   L   L   P   P   P   C   P   A   S   F   N   A   D   E   D   D
ACG GAG CTC ATC CTG CTG CCC CCT CCG TGC CCT GCC AGT TTC AAT GCG GAT GAG GAC GAT
 R   V   D   I   L   G   P   Q   P   E   S   H   Q   Q   L   S   A   S   S   H
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Fig. 5

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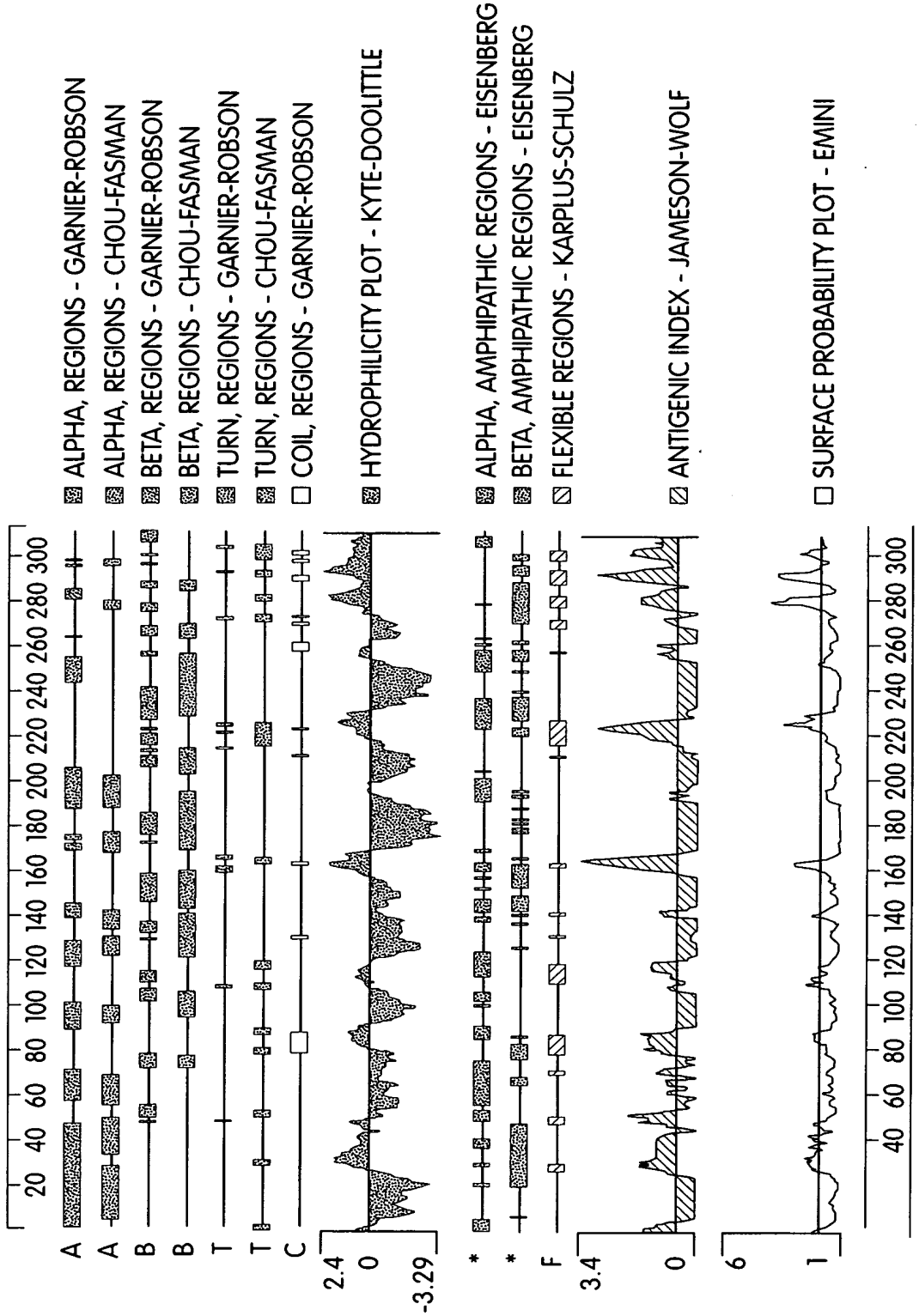
Fig. 5 (continued)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TURN, REGIONS - CHOU-FASMAN
COIL, REGIONS - GARNIER-ROBSON
HYDROPHILICITY PLOT - KYTE-DOOLITTLE
ALPHA, AMPHIPATHIC REGIONS - EISENBERG
BETA, AMPHIPATHIC REGIONS - EISENBERG
FLEXIBLE REGIONS - KARPLUS-SCHULZ
ANTIGENIC INDEX - JAMESON-WOLF
SURFACE PROBABILITY PLOT - EMINI
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A
B
B
T
T
C
2.4
0
-3.29
*
*
F
3.4
0
6
1
40 60 80 100 120 140 160 180 200 220 240 260 280 300

Fig. 6

Clustal W (1.74) multiple sequence alignment

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mTRAAK          ----------------------MRSTTLLALLAL-----------------VLLYLVS
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Athual33f10     ------MYRPRARAAPEGRVRGCAVPGTVLLLLAY-----------------LAYLAL
FthKa20g4       ---------------------MVDRGPLLTSAIIF-----------------YLAI
hTASK           ---------------------MKRQNVRTLALIVC-----------------TFTYLLV
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mTREK-1         GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS
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FthKa20g4       GAAIFEVLEEPHWKEAKKNYYTQKLHLLKEFPCLGQEGLDKILEVVSDAAGQGVAITGNQ
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                *: :.  :*                    :    :    : :   :           .

AthTb005e07     SGSANASDPAWDFASALFFASTLITTVGYGYTTPLTDAGKAFSIAFALLGVPTTMLLLTA
hTWIK-1         SGNWN-----WDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIPFTLLFLTA
mTRAAK          TNSSNHSS-AWNLGSAFFFSGTIITTIGYGNIVLHTDAGRLFCIFYALVGIPLFGMLLAG
mTREK-1         SNQVSH----WDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAG
Athual33f10     TSMGR-----WELVGSFFFSVSTITTIGYGNLSPNTMAARLFCIFFALVGIPLNLVVLNR
FthKa20g4       TFN-N-----WNWPNAMIFAATVITTIGYGNVAPKTPAGRLFCVFYGLFGVPLCLTWISA
hTASK           ----------WRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPLTLVMFQS
                          *   .:: *: : ::* *:*     : ..: *.: :.:.*:*     :

AthTb005e07     SAQRLSLLLTH--VPLSWLSMRWGWDPRRAACWHLVALLGVVVTVCFLVPAVIFAHLEEA
hTWIK-1         VVQRITVHVTR--RPVLYFHIRWGFSKQVVAIVHAVLLGFVTVSCFFFIPAAVFSVLEDD
mTRAAK          VGDRLGSSLRRGIGHIEAIFLKWHVPPGLVRSLSAVLFLLIGCLLFVLTPTFVFSYMES-
mTREK-1         VGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHIEG-
Athual33f10     LGHLMQQGVNH---WASRLGGTWQD-PDKARWLAGSGALLSGLLLFLLLPPLLFSHMEG-
FthKa20g4       LGKFFGGRAKR----LGQFLTKRGVSLRKAQITCTVIFIVWGVLVHLVIPPFVFMVTEG-
hTASK           LGERINTLVRY---LLHRAKKGLGMRRADVSMANMVLIGFFSCISTLCIGAAAFSHYEH-
                  . :                                          .   .  *   *

AthTb005e07     WSFLDAFYFCFISLSTIGLGDYVPGEAPGQ-----PYRALYKVLVTVYLFLGLVAMVLVL
hTWIK-1         WNFLESFYFCFISLSTIGLGDYVPGEGYNQ-----KFRELYKIGITCYLLLGLIAMLVVL
mTRAAK          WSKLEAIYFVIVTLTTVGFGDYVPGDGTGQNS-P-AYQPLVWFWILFGLAYFASVLTTIG
mTREK-1         WSALDAIYFVVITLTTIGFGDYVAGGSDIEYL-D-FYKPVVWFWILVGLAYFAAVLSMIG
Athual33f10     WSYTEGFYFAFITLSTVGFGDYVIGMNPSQRYPL-WYKNMVSLWILFGMAWLALIIKLIL
FthKa20g4       WNYIEGLYYSFITISTIGFGDFVAGVNPSANYHA-LYRYFVELWIYLGLAWLSLFVNWKV
hTASK           WTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIGAFLNLVV
                *.  :. *: .:::::*:*:**:*             :  .  . :   :      :

AthTb005e07     QTFRHVSDLHGLTELILLPPP----------------------------------------
hTWIK-1         ETFCELHELKKFRKMFYVKKDK-------------------------------------
mTRAAK          NWLRAVSRRTRAEMGGLTAQAA-------------------------------------
mTREK-1         DWLRVISKKTKEEVGEFRAHAA-------------------------------------
Athual33f10     SQLETPGRVCSCCHHSSKEDFK-------------------------------------
FthKa20g4       SMFVEVHKAIKKRRRRRKESFESSPHSRKALQVKGSTASKDVNIFSFLSKKEETYNDLIK
hTASK           LRFMTMNAEDEKRDAEHRALLTRN-----------------------------------
                  :
```

Fig. 7

```
AthTb005e07  ------------------------------------CPASFNADEDDRV--------
hTWIK-1      ------------------------------------DEDQVHIIEHDQLSFSSIT--
mTRAAK       ------------------------------------SWTGTVTARVTQR-----T--
mTREK-1      ------------------------------------EWTANVTAEFKETR----R--
Athua133f10  ------------------------------------SQSWRQGPDREPES---HS--
FthKa20g4    QIGKKAMKTSGGGETGPGPGLGPQGGGLPALPPSLVPLVVYSKNRVPTLEEVSQTLRSKG
hTASK        ------------------------------------GQAGGGGGGGSAHTTDTAS--

AthTb005e07  -DILGPQPESHQQ---LSASSHTDYASIPR----------------------------
hTWIK-1      -DQAAGMKEDQKQNEPFVATQSSACVDGPANH----------------------------
mTRAAK       -GPSAPPPEKEQPLLPSSLPAPPAVVEPAGRPGSPA-PAEKVETPSPPTA-SALDYPSEN
mTREK-1      -RLSVEIYDKFQR---ATSVKRKLSAELAGNHNQELTPCMRTCL----------------
Athua133f10  -PQQGCYPEGPMG--IIQHLEPSAHAAGCGKDS----------------------------
FthKa20g4    HVSRSPDEEAVARAPEDSSPAPEVFMNQLDRISEECEPWDAQDYHPLIFQ-DASITFVNT
hTASK        -STAAAGGGGFRNVYAEVLHFQSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEQSHS

AthTb005e07  ------------------------------------------------------------
hTWIK-1      ------------------------------------------------------------
mTRAAK       LAFIDESSDTQSERGCALPRAPRGRRRPNPSKKPSRPRGPGRLRDKAVPV----------
mTREK-1      ------------------------------------------------------------
Athua133f10  ------------------------------------------------------------
FthKa20g4    EAGLSDEETSKSSLEDNLAGEESPQQGAEAKAPLNMGEFPSSSESTFTSTESELSVPYEQ
hTASK        SPGGGGRYSDTPSRRCLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV----------

AthTb005e07  --------------
hTWIK-1      --------------
mTRAAK       --------------
mTREK-1      --------------
Athua133f10  --------------
FthKa20g4    LMNEYNKANSPKGT
hTASK        --------------
```

Fig. 7 (continued)

Clustal W (1.74) multiple sequence alignment

```
hTWIK-1       -------MLQSLAGSSCVRLVERHRSAWCFGFLVLG----------------YLLYLVF
AthTb005e07   ----------------------MRRGALLAGALAA----------------YAAYLVL
mTRAAK        ----------------------MRSTTLLALLAL----------------VLLYLVS
mTREK-1       MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVVLYLII
hTASK         --------------------MKRQNVRTLALIVC----------------TFTYLLV
                                   : .   . :                    **:

hTWIK-1       GAVVFSSVELPYEDLLRQELRKLKRRFLEEHECLSEQQLEQFLGRVLEASNYGVSVLSNA
AthTb005e07   GALLVARLEGPHEARLRAELETLRAQLLQRSPCVAAPALDAFVERVLAAGRLGRVVLANA
mTRAAK        GALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLEDFIKLLVEALGGGANPETSW
mTREK-1       GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS
hTASK         GAAVFDALESEPELIERQRLEL-RQQELRARYNLSQGGYEELERVVLRLKPHKAGVQ---
              ** :.  :*   *   :  :   :   :     :  :   ::

hTWIK-1       SGNWN-----WDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIPFTLLFLTA
AthTb005e07   SGSANASDPAWDFASALFFASTLITTVGYGYTTPLTDAGKAFSIAFALLGVPTTMLLLTA
mTRAAK        TNSSNHSS-AWNLGSAFFFSGTIITTIGYGNIVLHTDAGRLFCIFYALVGIPLFGMLLAG
mTREK-1       SNQVSH----WDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAG
hTASK         ----------WRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPLTLVMFQS
                        * : .:::*: *:::* *:*     ::.*: *.: ::::*:*   .:: .

hTWIK-1       VVQRITVHVTR--RPVLYFHIRWGFSKQVVAIVHAVLLGFVTVSCFFFIPAAVFSVLEDD
AthTb005e07   SAQRLSLLLTH--VPLSWLSMRWGWDPRRAACWHLVALLGVVVTVCFLVPAVIFAHLEEA
mTRAAK        VGDRLGSSLRRGIGHIEAIFLKWHVPPGLVRSLSAVLFLLIGCLLFVLTPTFVFSYMES-
mTREK-1       VGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHIEG-
hTASK         LGERINTLVRY---LLHRAKKGLGMRRADVSMANMVLIGFFSCISTLCIGAAAFSHYEH-
                :::   .     :                    : :  .    .  :  *   *

hTWIK-1       WNFLESFYFCFISLSTIGLGDYVPGEGYNQ-----KFRELYKIGITCYLLLGLIAMLVVL
AthTb005e07   WSFLDAFYFCFISLSTIGLGDYVPGEAPGQ-----PYRALYKVLVTBYLFLGLVAMVLVL
mTRAAK        WSKLEAIYFVIVTLTTVGFGDYVPGDGTGQNS--PAYQPLVWFWILFGLAYFASVLTTIG
mTREK-1       WSALDAIYFVVITLTTIGFGDYVAGGSDIEYL--DFYKPVVWFWILVGLAYFAAVLAMIG
hTASK         WTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIGAFLNLVV
              *. ::: *: .::*:*:*:****.          :  .  . :  *     :  :

hTWIK-1       ETFCELHELKKFRKMFYVKKDK--DEDQVHIIEHDQLSFSSITDQAAGMKEDQKQNEPFV
AthTb005e07   QTFRHVSDLHGLTELILLPPP---CPASFNADEDDRV------DILGPQPESHQQ---LS
mTRAAK        NWLRAVSRRTRAEMGGLTAQAA--SWTGTVTARVTQR-----TGPSAPPPEKEQPLLPSS
mTREK-1       DWLRVISKKTKEEVGEFRAHAA--EWTANVTAEFKETR----RRLSVEIYDKFQR---AT
hTASK         LRFMTMNAEDEKRDAEHRALLTRNGQAGGGGGGGSAHTTDTASSTAAAGGGGTRNVYAEV
                :  :                                          :

hTWIK-1       ATQSSACVDGPANH----------------------------------------------
AthTb005e07   ASSHTDYASIPR------------------------------------------------
mTRAAK        LPAPPAVVEPAGRPGSPA-PAEKVETPSPPTASALDYPSENLA-FIDESSDTQSERGCAL
mTREK-1       SVKRKLSAELAGNHNQELTPCMRTCL---------------------------------
hTASK         LHFQSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEQSHSSPGGGGRYSDTPSRRCLC

hTWIK-1       --------------------------------
AthTb005e07   --------------------------------
mTRAAK        PRAPRGRRRPNPSKKPSRPRGPGRLRDKAVPV
mTREK-1       --------------------------------
hTASK         SGAPRSAISSVSTGLHSLSTFRGLMKRRSSV-
```

Fig. 8

Clustal w (1.74) multiple sequence alignment

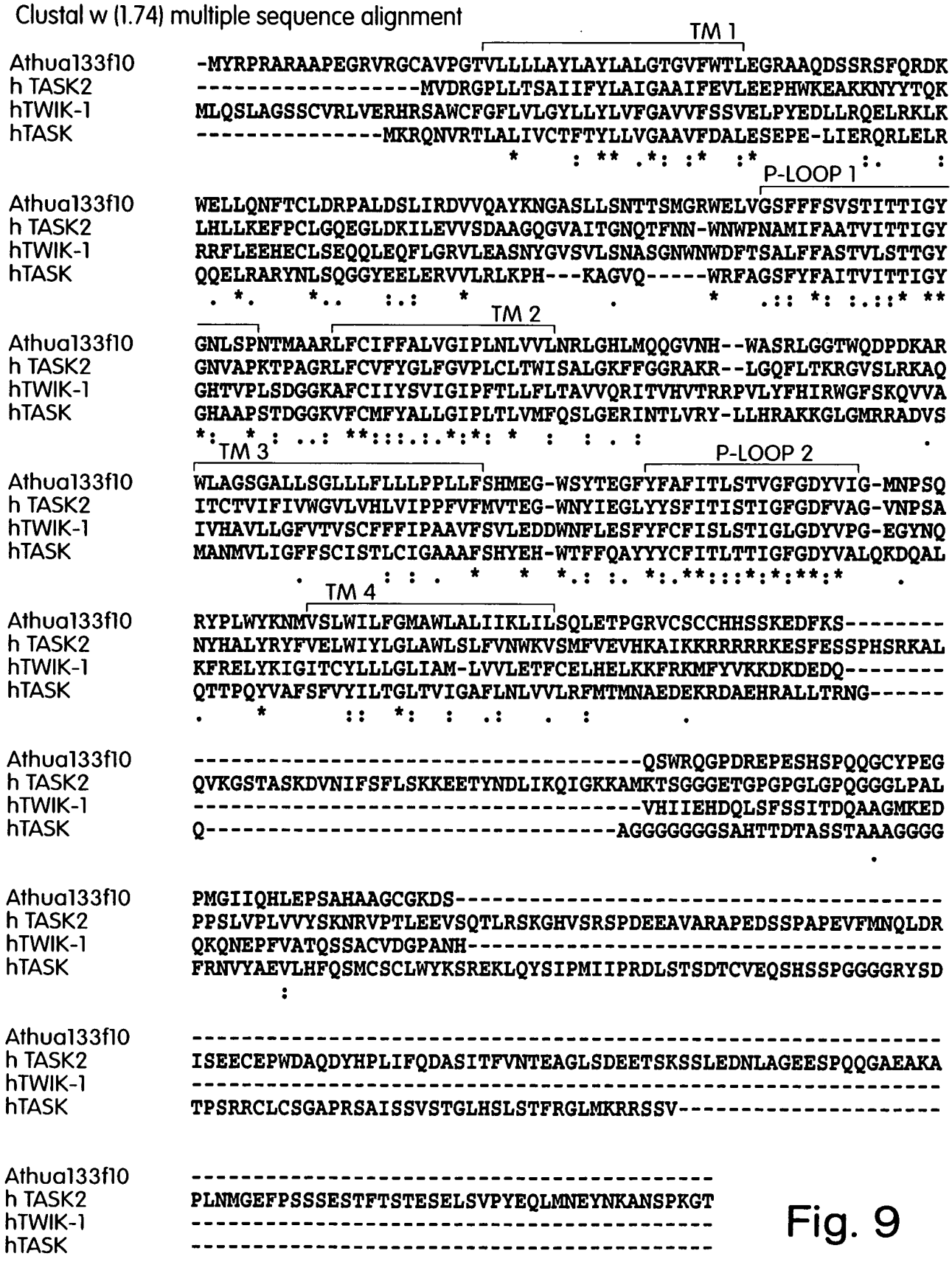

Fig. 9

```
 GAP of: twik2.pep  check: 1565  from: 1  to: 499

TWIK2 FthKa20g4

 to: twik3.pep  check: 8445  from: 1  to: 332

TWIK3 Athua133f10 - jthua133f10, 1575 bases, 18 checksum.

 Symbol comparison table:
/usr/local/gcg_9.1/gcgcore/data/rundata/blosum62.cmp
 CompCheck: 6430

        Gap Weight:     12      Average Match:  2.912
     Length Weight:      4   Average Mismatch: -2.003

           Quality:    396             Length:    517
             Ratio:  1.193              Gaps:      3
 Percent Similarity: 40.764   Percent Identity: 32.166

       Match display thresholds for the alignment(s):
                  | = IDENTITY
                  : =   2
                  . =   1

 twik2.pep x twik3.pep

                .         .         .         .         .
      1 .................MVDRGPLLTSAIIFYLAIGAAIFEVLEEPHWKE 33
                           |    ||  | : |||:|  :|  ||    .:
      1 MYRPRARAAPEGRVRGCAVPGTVLLLLAYLAYLALGTGVFWTLEGRAAQD 50
                .         .         .         .         .
     34 AKKNYYTQKLHLLKEFPCLGQEGLDKILEVVSDAAGQGVAITGNQT.FNN 82
        . :.:   |  ||. | || .  || ::  |  |   | .:  | |
     51 SSRSFQRDKWELLQNFTCLDRPALDSLIRDVVQAYKNGASLLSNTTSMGR 100
                .         .         .         .         .
     83 WNWPNAMIFAATVITTIGYGNVAPKTPAGRLFCVFYGLFGVPLCLTWISA 132
        |    .  |. . |||||||||..| | | ||||:|: | |:|| |  :.
    101 WELVGSFFFSVSTITTIGYGNLSPNTMAARLFCIFFALVGIPLNLVVLNR 150
                .         .         .         .         .
    133 LGKFFGGRAKRLGQFLTKRGVSLRKAQITCTVIFIVWGVLVHLVIPPFVF 182
        ||              |        ||.       :. |.|. |.:|| .|
    151 LGHLMQQGVNHWASRLGGTWQDPDKARWLAGSGALLSGLLLFLLLPPLLF 200
                .         .         .         .         .
    183 MVTEGWNYIEGLYYSFITISTIGFGDFVAGVNPSANYHALYRYFVELWIY 232
           |||.| || |:.|||:||:||||:| |.|||  |   |:  | |||
    201 SHMEGWSYTEGFYFAFITLSTVGFGDYVIGMNPSQRYPLWYKNMVSLWIL 250
                .         .         .         .         .
    233 LGLAWLSLFVNWKVSMFVEVHKAIKKRRRRRKESFESSPHSRKALQVKGS 282
         |:|||.| :   .|      :          || |.|    |.    .
    251 FGMAWLALIIKLILSQLETPGRVCSCCHHSSKEDFKSQSW.RQGPDREPE 299
                .         .         .         .         .
    283 TASKDVNIFSFLSKKEETYNDLIKQIGKKAMKTSGGGETGPGPGLGPQGG 332
        . |     :        |    :|. :   |       | :.
    300 SHSPQQGCY......PEGPMGIIQHLEPSAHAAGCGKDS..........  332
                          .
                          :
                          .
```

Fig. 10

```
 GAP of: twik4.pep  check: 9188  from: 1  to: 313

TWIK4 AthTb005e07 - jthTb005e07, 2287 bases, 4935 checksum.

 to: twik2.pep  check: 1565  from: 1  to: 499

TWIK2 FthKa20g4

 Symbol comparison table:
/usr/local/gcg_9.1/gcgcore/data/rundata/blosum62.cmp
 CompCheck: 6430

        Gap Weight:     12      Average Match:  2.912
     Length Weight:      4   Average Mismatch: -2.003

           Quality:    221             Length:    512
             Ratio:  0.706               Gaps:      5
Percent Similarity: 37.667   Percent Identity: 27.333

       Match display thresholds for the alignment(s):
                   | = IDENTITY
                   : =   2
                   . =   1

twik4.pep x twik2.pep..

      1 .MRRGALLAGALAAYAAYLVLGALLVARLEGPHEARLRAELETLRAQLLQ 49
        . || ||  |:     || :|| :   || ||    :    | :  ||.
      1 MVDRGPLLTSAI...IFYLAIGAAIFEVLEEPHWKEAKKNYYTQKLHLLK 47

     50 RSPCVAAPALDAFVERVLAAGRLGRVVLANASGSANASDPAWDFASALFF 99
        ||.    ||  .| |  |   |  :  | . .      |.. .|: |
     48 EFPCLGQEGLDKILEVVSDAAGQGVAITGNQTFN.....NWNWPNAMIF 91

    100 ASTLITTVGYGYTTPLTDAGKAFSIAFALLGVPTTMLLLTASAQRLSLLL 149
        |.|.|||:|||   | | ||: | : : | |||  :  :.|  .
     92 AATVITTIGYGNVAPKTPAGRLFCVFYGLFGVPLCLTWISALGKFFGGRA 141

    150 THVPLSWLSMRWGWDPRRAACWHLVALLGVVVTVCFLVPAVIFAHLEEAW 199
          |     : |   |:|     |  :   | |  .:|  :|  . | |
    142 KR..LGQFLTKRGVSLRKAQITCTVIFIVWGVLVHLVIPPFVFM.VTEGW 188

    200 SFLDAFYFCFISLSTIGLGDYVPGEAPGQPYRALYKVLVTVYLFLGLVAM 249
        .:::  |: ||.:|||| ||:| |   |   | |||:  | .:::||| |
    189 NYIEGLYYSFITISTIGFGDFVAGVNPSANYHALYRYFVELWIYLGL.AW 237

    250 VLVLQTFRHVSDLHGLTELILLPPPCPASFNADEDDRVDILGPQPESHQQ 299
        . .  .:   .    :          || .   |  :      . .
    238 LSLFVNWKVSMFVEVHKAIKKRRRRRKESFESSPHSRKALQVKGSTASKD 287

    300 LSASSHTDYASIPR..............................  313
        ..  |
    288 VNIFSFLSKKEETYNDLIKQIGKKAMKTSGGGETGPGPGLGPQGGGLPAL 337
```

Fig. 11

```
 GAP of: twik3.pep  check: 8445  from: 1  to: 332

TWIK3 Athua133f10 - jthua133f10, 1575 bases, 18 checksum.

 to: twik4.pep  check: 9188  from: 1  to: 313

TWIK4 AthTb005e07 - jthTb005e07, 2287 bases, 4935 checksum.

 Symbol comparison table:
/usr/local/gcg_9.1/gcgcore/data/rundata/blosum62.cmp
 CompCheck: 6430

        Gap Weight:     12      Average Match:  2.912
     Length Weight:      4   Average Mismatch: -2.003

           Quality:    257             Length:    345
             Ratio:  0.821              Gaps:      7
Percent Similarity: 40.333   Percent Identity: 31.667

       Match display thresholds for the alignment(s):
                   | = IDENTITY
                   : =   2
                   . =   1

 twik3.pep x twik4.pep..

                .         .         .         .         .
      1 MYRPRARAAPEGRVRGCAVPGTVLLLLAYLAYLALGTGVFWTLEGRAAQD 50
                  ||  . |    | ||| ||| ||  .   |||
      1 ............MRRGALLAGA...LAAYAAYLVLGALLVARLEGPHEAR 35
                .         .         .         .         .
     51 SSRSFQRDKWELLQNFTCLDRPALDSLIRDVVQAYKNGASLLSNTTSMGR 100
           :  : :|||   |.  ||||. :  |. | : |  .|.| .
     36 LRAELETLRAQLLQRSPCVAAPALDAFVERVLAAGRLGRVVLANASGSAN 85
                .         .         .         .         .
    101 .....WELVGSFFFSVSTITTIGYGNLSPNTMAARLFCIFFALVGIPLNL 145
           |:   . ||. . |||:|||  .| | | : | | |||.|:|  :
     86 ASDPAWDFASALFFASTLITTVGYGYTTPLTDAGKAFSIAFALLGVPTTM 135
                .         .         .         .         .
    146 VVLNRLGHLMQQGVNHW.ASRLGGTW.QDPDKARWLAGSGALLSGLLLFL 193
        ..|      :   . |   | |   |  || :|        |   . .
    136 LLLTASAQRLSLLLTHVPLSWLSMRWGWDPRRAACWHLVALLGVVVTVCF 185
                .         .         .         .         .
    194 LLPPLLFSHM.EGWSYTEGFYFAFITLSTVGFGDYVIGMNPSQRYPLWYK 242
        |.| .:|.|: | ||: : ||| ||.|||:| ||||| |  | | |   ||
    186 LVPAVIFAHLEEAWSFLDAFYFCFISLSTIGLGDYVPGEAPGQPYRALYK 235
                .         .         .         .         .
    243 NMVSLWILFGMAWLALIIKLILSQLETPG.....RVCSCCHHSSKEDFKS 287
         :|..::  |:  : |::.      : |       .   |  |   |
    236 VLVTVYLFLGLVAMVLVLQTFRHVSDLHGLTELILLPPPCPASFNADEDD 285
                .         .         .         .
    288 QSWRQGPDREPESHSPQQGCYPEGPMGIIQHLEPSAHAAGCGKDS 332
        .   ||  :||||              | .
    286 RVDILGP..QPESHQQLSASSHTDYASIPR.............. 313
```

Fig. 12

```
 GAP of: htwik-1.pep  ch ck: 4093  from: 1  to: 336

hTWIK-1 U33632 Human two P-domain K+ channel TWIK-1 mRNA, complete cds.

 to: twik2.pep  check: 1565  from: 1  to: 499

TWIK2 FthKa20g4

 Symbol comparison table:
/usr/local/gcg_9.1/gcgcore/data/rundata/blosum62.cmp
 CompCheck: 6430

        Gap Weight:     12      Average Match:  2.912
     Length Weight:      4   Average Mismatch: -2.003

           Quality:    269             Length:    521
             Ratio:  0.801               Gaps:      4
 Percent Similarity: 36.943   Percent Identity: 26.433

       Match display thresholds for the alignment(s):
                   | = IDENTITY
                   : =   2
                   . =   1
 htwik-1.pep x twik2.pep
                .         .         .         .         .
      1 MLQSLAGSSCVRLVERHRSAWCFGFLVLGYLLYLVFGAVVFSSVELPYED 50
                                    |    : ||  || :|  .| |:
      1 ..................MVDRGPLLTSAIIFYLAIGAAIFEVLEEPHWK 32
                .         .         .         .         .
     51 LLRQELRKLKRRFLEEHECLSEQQLEQFLGRVLEASNYGVSVLSNASGNW 100
          :.     |   |.|  || :: |:. |  | :|.  ||.:  | . |
     33 EAKKNYYTQKLHLLKEFPCLGQEGLDKILEVVSDAAGQGVAITGNQTFN. 81
                .         .         .         .         .
    101 NWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIPFTLLFLT 150
         ||.. .|: ||.||:.| |||.  | .  |: ||: | . |:|  | .:.
     82 NWNWPNAMIFAATVITTIGYGNVAPKTPAGRLFCVFYGLFGVPLCLTWIS 131
                .         .         .         .         .
    151 AVVQRITVHVTRRPVLYFHIRWGFSKQVVAIVHAVLLGFVTVSCFFFIPA 200
         |. .       |  .  |  : | | .   |   |:     |      ||
    132 ALGKFFGGRAKR..LGQFLTKRGVSLRKAQITCTVIFIVWGVLVHLVIPP 179
                .         .         .         .         .
    201 AVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELYKIGIT 250
         || | |  ||::|  |: ||.:|||| ||:| |   .  :  ||:  :
    180 FVFMVTE.GWNYIEGLYYSFITISTIGFGDFVAGVNPSANYHALYRYFVE 228
                .         .         .         .         .
    251 CYLLLGL..IAMLVVLETFCELHELKKFRKMFYVKKDKDEDQVHIIEHDQ 298
         :: |||  :.: |  .    .   |  :|    :|:  |   |  .  |
    229 LWIYLGLAWLSLFVNWKVSMFVEVHKAIKKRRRRRKESFESSPHSRKALQ 278
                .         .         .         .         .
    299 LSFSSITDQAAGMKEDQKQNEPFVATQSSACVDGPANH..........  336
         .  |. .           |. | :
    279 VKGSTASKDVNIFSFLSKKEETYNDLIKQIGKKAMKTSGGGETGPGPGLG 328
                                  .
                                  :
                                  .
```

Fig. 13

```
 GAP of: htwik-1.pep  check: 4093  from: 1  to: 336

hTWIK-1 U33632 Human two P-domain K+ channel TWIK-1 mRNA, complete cds.

 to: twik3.pep  check: 8445  from: 1  to: 332

TWIK3 Athua133f10 - jthua133f10, 1575 bases, 18 checksum.

 Symbol comparison table:
/usr/local/gcg_9.1/gcgcore/data/rundata/blosum62.cmp
 CompCheck: 6430

        Gap Weight:     12      Average Match:  2.912
     Length Weight:      4   Average Mismatch: -2.003

           Quality:    199             Length:    337
             Ratio:  0.599              Gaps:      3
 Percent Similarity: 31.420   Percent Identity: 22.961

       Match display thresholds for the alignment(s):
                  | = IDENTITY
                  : =   2
                  . =   1

 htwik-1.pep x twik3.pep..
```

```
          .         .         .         .         .
  1 MLQSLAGSSCVRLVERHRSAWCFGFLVLGYLLYLVFGAVVFSSVELPYED 50
    :       .       |  .      |.| || || |  || ..|
  1 .MYRPRARAAPEGRVRGCAVPGTVLLLLAYLAYLALGTGVFWTLEGRAAQ 49

          .         .         .         .         .
 51 LLRQELRKLKRRFLEEHECLSEQQLEQFLGRVLEASNYGVSVLSNASGNW 100
       .  .: |    |:   ||    |:  :  |.:|   | |.||| .
 50 DSSRSFQRDKWELLQNFTCLDRPALDSLIRDVVQAYKNGASLLSNTTSMG 99

          .         .         .         .         .
101 NWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIPFTLLFLT 150
     |:   . ||. . :.| |||.  | .   : ||| :..:|||  |. |
100 RWELVGSFFFSVSTITTIGYGNLSPNTMAARLFCIFFALVGIPLNLVVLN 149

          .         .         .         .         .
151 AVVQRITVHVTRRPVLYFHIRWGFSKQVVAIVHAVLLGFVTVSCFFFIPA 200
     .   .  |              |           ||  . .  |  :|
150 RLGHLMQQGVNHWASRLGGTWQDPDKARWLAGSGALLSGLLL..FLLLPP 197

          .         .         .         .         .
201 AVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELYKIGIT 250
     .|| :|  |.: | ||| ||.|||:| ||||| |   .|::   ||  :.
198 LLFSHME.GWSYTEGFYFAFITLSTVGFGDYVIGMNPSQRYPLWYKNMVS 246

          .         .         .         .         .
251 CYLLLGLIAMLVVLE.TFCELHELKKFRKMFYVKKDKDEDQVHIIEHDQL 299
     ::| |:  : .:::.    :|    :    :    .|       :
247 LWILFGMAWLALIIKLILSQLETPGRVCSCCHHSSKEDFKSQSWRQGPDR 296

          .         .         .
300 SFSSITDQAAGMKEDQKQNEPFVATQSSACVDGPANH 336
       | . |     |         .   . |   | .
297 EPESHSPQQGCYPEGPMGIIQHLEPSAHAAGCGKDS. 332
```

Fig. 14

```
 GAP of: htwik-1.pep  check: 4093  from: 1  to: 336

hTWIK-1 U33632 Human two P-domain K+ channel TWIK-1 mRNA, complete cds.

 to: twik4.pep  check: 9188  from: 1  to: 313

TWIK4 AthTb005e07 - jthTb005e07, 2287 bases, 4935 checksum.

 Symbol comparison table:
/usr/local/gcg_9.1/gcgcore/data/rundata/blosum62.cmp
 CompCheck: 6430

        Gap Weight:     12      Average Match:  2.912
     Length Weight:      4   Average Mismatch: -2.003

           Quality:    575             Length:    353
             Ratio:  1.837               Gaps:      4
Percent Similarity: 55.405   Percent Identity: 46.284

       Match display thresholds for the alignment(s):
                  | = IDENTITY
                  : =   2
                  . =   1

htwik-1.pep x twik4.pep..

      1 MLQSLAGSSCVRLVERHRSAWCFGFLVLGYLLYLVFGAVVFSSVELPYED 50
                        | |   | |   |  ||| ||.. . .| |:|
      1 ...............MRRGALLAGALA.AYAAYLVLGALLVARLEGPHEA 34

     51 LLRQELRKLKRRFLEEHECLSEQQLEQFLGRVLEASNYGVSVLSNASGNW 100
        || ||  |: . |:   |..   |: |. ||| |   |  ||.||||.
     35 RLRAELETLRAQLLQRSPCVAAPALDAFVERVLAAGRLGRVVLANASGSA 84

    101 N.....WDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIPFT 145
        |     ||| |||||||||.:.| |||:| ||.| |||| | :..:|:| |
     85 NASDPAWDFASALFFASTLITTVGYGYTTPLTDAGKAFSIAFALLGVPTT 134

    146 LLFLTAVVQRITVHVTRRPVLYFHIRWGFSKQVVAIVHAVLLGFVTVSCF 195
        :| |||  ||:.. .|  |. :  .|||.  .  |  | | |  | |.
    135 MLLLTASAQRLSLLLTHVPLSWLSMRWGWDPRRAACWHLVALLGVVVTVC 184

    196 FFIPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELY 245
        | :|| :|. ||: |.||:.|||||||||||||||||||||   | :| ||
    185 FLVPAVIFAHLEEAWSFLDAFYFCFISLSTIGLGDYVPGEAPGQPYRALY 234

    246 KIGITCYLLLGLIAMLVVLETFCELHELKKFRKMFYVK.......KDKDE 288
        |: :| || |||:||..||:||  . :|    .:  .           ::
    235 KVLVTVYLFLGLVAMVLVLQTFRHVSDLHGLTELILLPPPCPASFNADED 284

    289 DQVHII.....EHDQLSFSSITDQAAGMKEDQKQNEPFVATQSSACVDGP 333
        |.| |:       | ||| || || |.  :
    285 DRVDILGPQPESHQQLSASSHTDYASIPR..................... 313
```

Fig. 15

```
GAP of: htask2.pep  check: 1565  from: 1  to: 499

hTASK2 3925427 in GenPept

 to: twik2.pep  check: 1565  from: 1  to: 499

TWIK2 FthKa20g4

 Symbol comparison table:
/usr/local/gcg_9.1/gcgcore/data/rundata/blosum62.cmp
 CompCheck: 6430

        Gap Weight:     12      Average Match:  2.912
     Length Weight:      4   Average Mismatch: -2.003

           Quality:   2613             Length:    499
             Ratio:  5.236               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

       Match display thresholds for the alignment(s):
                  | = IDENTITY
                  : =   2
                  . =   1
 htask2.pep x twik2.pep..

        1 MVDRGPLLTSAIIFYLAIGAAIFEVLEEPHWKEAKKNYYTQKLHLLKEFP 50
          ||||||||||||||||||||||||||||||||||||||||||||||||||
        1 MVDRGPLLTSAIIFYLAIGAAIFEVLEEPHWKEAKKNYYTQKLHLLKEFP 50

       51 CLGQEGLDKILEVVSDAAGQGVAITGNQTFNNWNWPNAMIFAATVITTIG 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||
       51 CLGQEGLDKILEVVSDAAGQGVAITGNQTFNNWNWPNAMIFAATVITTIG 100

      101 YGNVAPKTPAGRLFCVFYGLFGVPLCLTWISALGKFFGGRAKRLGQFLTK 150
          ||||||||||||||||||||||||||||||||||||||||||||||||||
      101 YGNVAPKTPAGRLFCVFYGLFGVPLCLTWISALGKFFGGRAKRLGQFLTK 150

      151 RGVSLRKAQITCTVIFIVWGVLVHLVIPPFVFMVTEGWNYIEGLYYSFIT 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||
      151 RGVSLRKAQITCTVIFIVWGVLVHLVIPPFVFMVTEGWNYIEGLYYSFIT 200

      201 ISTIGFGDFVAGVNPSANYHALYRYFVELWIYLGLAWLSLFVNWKVSMFV 250
          ||||||||||||||||||||||||||||||||||||||||||||||||||
      201 ISTIGFGDFVAGVNPSANYHALYRYFVELWIYLGLAWLSLFVNWKVSMFV 250

      251 EVHKAIKKRRRRRKESFESSPHSRKALQVKGSTASKDVNIFSFLSKKEET 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||
      251 EVHKAIKKRRRRRKESFESSPHSRKALQVKGSTASKDVNIFSFLSKKEET 300

      301 YNDLIKQIGKKAMKTSGGGETGPGPGLGPQGGGLPALPPSLVPLVVYSKN 350
          ||||||||||||||||||||||||||||||||||||||||||||||||||
      301 YNDLIKQIGKKAMKTSGGGETGPGPGLGPQGGGLPALPPSLVPLVVYSKN 350
```

Fig. 16

```
351 RVPTLEEVSQTLRSKGHVSRSPDEEAVARAPEDSSPAPEVFMNQLDRISE 400
    ||||||||||||||||||||||||||||||||||||||||||||||||||
351 RVPTLEEVSQTLRSKGHVSRSPDEEAVARAPEDSSPAPEVFMNQLDRISE 400

401 ECEPWDAQDYHPLIFQDASITFVNTEAGLSDEETSKSSLEDNLAGEESPQ 450
    ||||||||||||||||||||||||||||||||||||||||||||||||||
401 ECEPWDAQDYHPLIFQDASITFVNTEAGLSDEETSKSSLEDNLAGEESPQ 450

451 QGAEAKAPLNMGEFPSSSESTFTSTESELSVPYEQLMNEYNKANSPKGT  499
    |||||||||||||||||||||||||||||||||||||||||||||||||
451 QGAEAKAPLNMGEFPSSSESTFTSTESELSVPYEQLMNEYNKANSPKGT  499
```

Fig. 16 (continued)

>human TWIK 5

CTAGGGAGGGCGCCATCTGAGTAGTTCGGAAGAACTGAACATGATGAGTT
GCCGGCTGCTTCCTGAGTCCTTGGGGAAGCACACGCACCATCCACTTAGC
ACTGGAGCCTGGCTGTTCTCCGGGCACTCCTACCCCATCTTCCTGGCGGG
GCTTAGATGCTCCTGCCTCTTCCACCAGCTCCTCTTGCCCTGCATGCTTC
AGGGACGATGGAGGTCTCGGGGCACCCCCAGGCCAGGAGATGCTGCCCAG
AGGCCCTGGGAAAGCTCTTCCCTGGCCTCTGCTTCCTCTGCTTTCTGGTG
ACCTACGCCCTGGTGGGTGCTGTGGTCTTCTCTGCCATTGAGGACGGCCA
GGTCCTGGTGGCAGCAGATGATGGAGAGTTTGAGAAGTTCTTGGAGGAGC
TCTGCAGAATCTTGAACTGCAGTGAAACAGTGGTGGAAGACAGAAAACAG
GATCTCCAGGGGCATCTGCAGAAGGTGAAGCCTCAGTGGTTTAACAGGAC
CACACACTGGTCCTTCCTGAGCTCGCTCTTTTTCTGCTGCACGGTGTTCA
GCACCGTGGGCTATGGCTACATCTACCCCGTCACCAGGCTTGGCAAGTAC
TTGTGCATGCTCTATGCTCTCTTTGGTATCCCCCTGATGTTCCTCGTTCT
CACGGACACAGGCGACATCCTGGCAACCATCTTATCTACATCTTATAATC
GGTTCCGAAAATTCCCTTTCTTTACCCGCCCCCTCCTCTCCAAGTGGTGC
CCCAAATCTCTCTTCAAGAAAAAACCGGACCCCAAGCCCGCAGATGAAGC
TGTCCCTCAGATCATCATCAGTGCTGAAGAGCTTCCAGGCCCCAAACTTG
GCACATGTCCTTCACGCCCAAGCTGCAGCATGGAGCTGTTTGAGAGATCT
CATGCGCTAGAGAAACAGAACACACTGCAACTGCCCCCACAAGCCATGGA
GAGGAGTAACTCGTGTCCCGAACTGGTGTTGGGAAGACTCTCATACTCCA
TCATCAGCAACCTGGATGAAGTTGGACAGCAGGTGGAGAGGTTGGACATC
CCCCTCCCCATCATTGCCCTTATTGTTTTTGCCTACATTTCCTGTGCAGC
TGCCATCCTCCCCTTCTGGGAGACACAGTTGGATTTCGAGAATGCCTTCT
ATTTCTGCTTTGTCACACTCACCACCATTGGGTTTGGGGATACTGTTTTA
GAACACCCTAACTTCTTCCTGTTCTTCTCCATTTATATCATCGTTGGAAT
GGAGATTGTGTTCATTGCTTTCAAGTTGGTGCAAAACAGGCTGATTGACA
TATACAAAAATGTTATGCTATTCTTTGCAAAAGGGAAGTTTTACCACCTT
GTTAAAAAGTGAAGGTTTCATTATCTCTCAGGTGACAGACACTGGCTGAG
CTGGTTTTCTTGTGTTGTCTTTCAGGGTCATGCAGCCTGTCACCTGAGAC
CTTCAGTCTTGGAGACAAATCCCTTATGAGAGCCAAGTTCAGTCTTGAGG
CCCTGC

MLLPLPPAPLALHASGTMEVSGHPQARRCCPEALGKLFPGLCFLCFLVTYALVGAVV
FSAIEDGQVLVAADDGEFEKFLEELCRILNCSETVVEDRKQDLQGHLQKVKPQWFNR
TTHWSFLSSLFFCCTVFSTVGYGYIYPVTRLGKYLCMLYALFGIPLMFLVLTDTGDI
LATILSTSYNRFRKFPFFTRPLLSKWCPKSLFKKKPDPKPADEAVPQIIISAEELPG
PKLGTCPSRPSCSMELFERSHALEKQNTLQLPPQAMERSNSCPELVLGRLSYSIISN
LDEVGQQVERLDIPLPIIALIVFAYISCAAAILPFWETQLDFENAFYFCFVTLTTIG
FGDTVLEHPNFFLFFSIYIIVGMEIVFIAFKLVQNRLIDIYKNVMLFFAKGKFYHLV
KK

Fig. 17

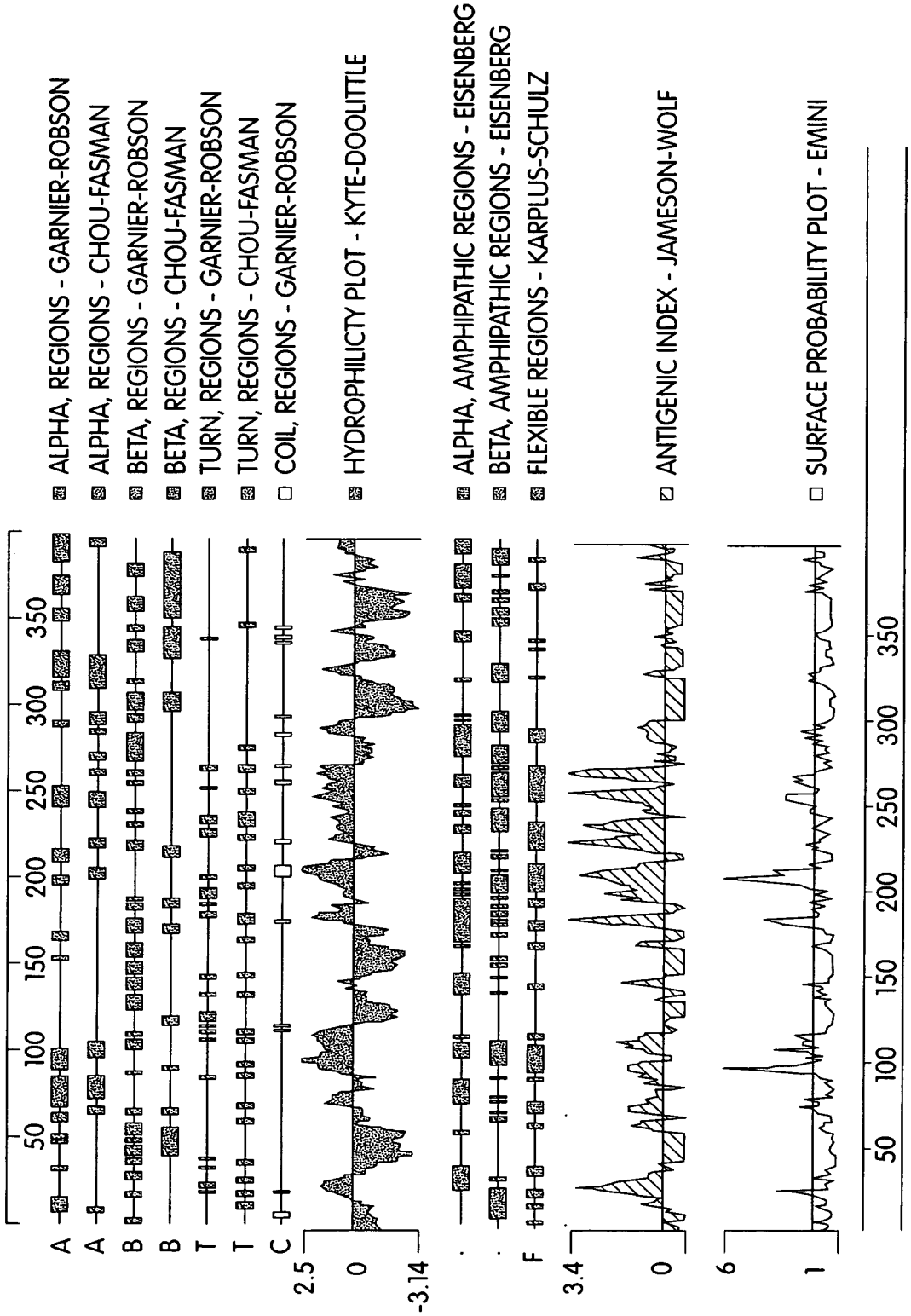
ALPHA, REGIONS - GARNIER-ROBSON
ALPHA, REGIONS - CHOU-FASMAN
BETA, REGIONS - GARNIER-ROBSON
BETA, REGIONS - CHOU-FASMAN
TURN, REGIONS - GARNIER-ROBSON
TURN, REGIONS - CHOU-FASMAN
COIL, REGIONS - GARNIER-ROBSON
HYDROPHILICTY PLOT - KYTE-DOOLITTLE
ALPHA, AMPHIPATHIC REGIONS - EISENBERG
BETA, AMPHIPATHIC REGIONS - EISENBERG
FLEXIBLE REGIONS - KARPLUS-SCHULZ
ANTIGENIC INDEX - JAMESON-WOLF
SURFACE PROBABILITY PLOT - EMINI
50
100
150
200
250
300
350
2.5
0
-3.14
3.4
0
6
1

Fig. 18

```
GAP of: ORBa005gy  ch ck: 9848  from: 1  to: 401

TWIK-5 protein (analysis onl - Import - compl t

to: PRBa005gy  check: 4672  from: 1  to: 394

2465542 in GenPept

Symbol comparison table: /prod/ddm/seqanal/BLAST/matrix/aa/PAM250
CompCheck: 5553

       Gap Weight:     25      Average Match:  2.617
    Length Weight:      1   Average Mismatch: -3.416

          Quality:    166             Length:    538
            Ratio:  0.421              Gaps:      5
Percent Similarity: 49.805   Percent Identity: 29.183

      Match display thresholds for the alignment(s):
                  | = IDENTITY
                  : =    2
                  . =    1

ORBa005gy x PRBa005gy

  1 MLLPLPPAPLALHASGTMEVSGHPQARRCCPEALGKLFPGLCFLCFLVTY 50
  1 ..............................MKRQNVRTLALIVCTFTY 18

 51 ALVGAVVFSAIEDGQVLVAADDGEFEKFLEELCRILNCSETVVEDRKQDL 100
 19 LLVGAAVFDALESEPELIERQRLELRQ......QELRARYNLSQGGYEEL 62

101 QGHLQKVKPQWFNRTTHWSFLSSLFFCCTVFSTVGYGYIYPVTRLGKYLC 150
 63 ERVVLRLKPH..KAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFC 110

151 MLYALFGIPLMFLVLTDTGDILATILSTSYNRFRKFPFFTRPLLSKWCPK 200
111 MFYALLGIPLTLVMFQSLGERINTLVRYLLHRAKK.............. 145

251 LEKQNTLQLPPQAMERSNSCPELVLGRLSYSIISNLDEVGQQVERLDIPL 300
146 ..................................GLGMRRADVSM 156

301 PIIALIVF...AYISCAAAILPFWETQLDFENAFYFCFVTLTTIGFGD.. 345
157 ANMVLIGFFSCISTLCIGAAAFSHYEHWTFFQAYYYCFITLTTIGFGDYV 206

346 ......TVLEHPNFFLFFSIYIIVGMEIVFIAFKLVQNRLIDIYKNVMLF 389
207 ALQKDQALQTQPQYVAFSFVYILTGLTVIGAFLNLVVLRFMTMNAEDEKR 256

390 FAKGKFYHLVKK..................................... 401
257 DAEHRALLTRNGQAGGGGGGGSAHTTDTASSTAAAGGGGFRNVYAEVLHF 306
```

Fig. 19

```
GAP of: GRBa005gy  ch ck: 9848  from: 1  to: 401
 TWIK-5 prot in (analysis onl - Import - complet
 to: HRBa005gy  check: 2856  from: 1  to: 426
 4101566 in GenPept

 Symbol comparison table: /prod/ddm/seqanal/BLAST/matrix/aa/PAM250
 CompCheck: 5553

        Gap Weight:     25      Average Match:  2.617
     Length Weight:      1   Average Mismatch: -3.416

           Quality:     77             Length:    563
             Ratio:  0.192               Gaps:      6
 Percent Similarity: 44.697   Percent Identity: 27.273

        Match display thresholds for the alignment(s):
                    | = IDENTITY
                    : =   2
                    . =   1

 GRBa005gy x HRBa005gy

                .         .         .         .         .
       1 ..............................MLLPLPPAPLALHASGTM 18
                                       |.:. | | | .
       1 MLPSASRERPGYRAGVAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVES 50
                 .         .         .         .         .
      19 EVSGHPQARRCCPEALGKLFPGLCFLCFLVTYALVGAVVFSAIEDGQVLV 68
         : . :   ::  .           .:  :| | ::|| || |:|: : :
      51 DTTINVMKWKTVST.........IFLVVVLYLIIGATVFKALEQPHEIS 90
                 .         .         .         .         .
      69 AADDGEFEK..FLEELCRILNCSETVVEDRKQDLQGHLQKVKPQWFNRTT 116
               .:|  |: :   : .     : :.           .  |. .
      91 QRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAINAGIIPLGNTSNQIS 140
                 .         .         .         .         .
     117 HWSFLSSLFFCCTVFSTVGYGYIYPVTRLGKYLCMLYALFGIPLMFLVLT 166
         || : ||:|| ||..|:|:| | | | || :|::|||:|||| ::|.
     141 HWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLA 190
                 .         .         .         .         .
     167 DTGDILATILSTSYNRFRKFPFFTRPLLSKWCPKSLFKKKPDPKPADEAV 216
         . ||| .||:. .
     191 GVGDQLGTIFGKG..................................... 203
                                    .
                                    .
                                    .
                 .         .         .         .         .
     267 SNSCPELVLGRLSYSIISNLDEVGQQVERLDIPLPIIALIVFAYISCA.. 314
                          |.:::  . .  :  : ||. |:|  ..|
     204 ................IAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLF 237
                 .         .         .         .         .
     315 ...AAILPFWETQLDFENAFYFCFVTLTTIGFGDTVLEHPNFFLFFSIYI 361
           .||:           :|.||  :|||||||||               |:
     238 VALPAIIFKHIEGWSALDAIYFVVITLTTIGFGD.............YV 273
                 .         .         .         .         .
     362 IVGMEIVFIAFKLVQNRLIDIYKNVMLFFAKGKFYHLVKK......... 401
           | :| :: |           |||| :|      :  :
     274 AGGSDIEYLDF.........YKPVVWFWILVGLAYFAAVLSMIGRLVRV 313
                                    .
                                    .
                                    .
```

Fig. 20

25/26

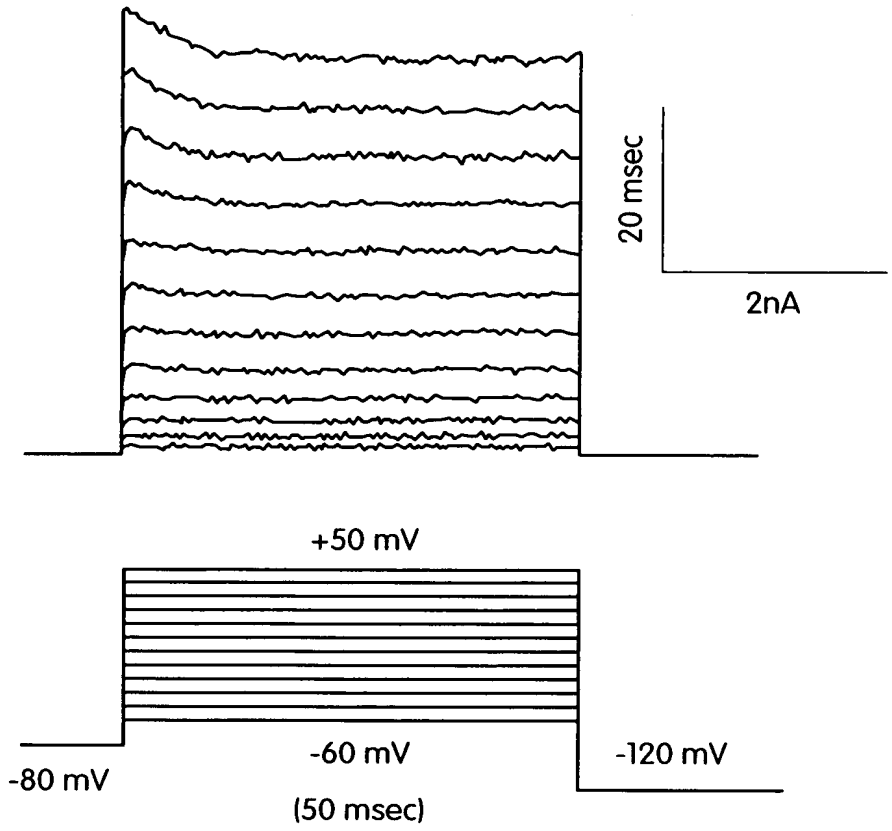

Fig. 21A

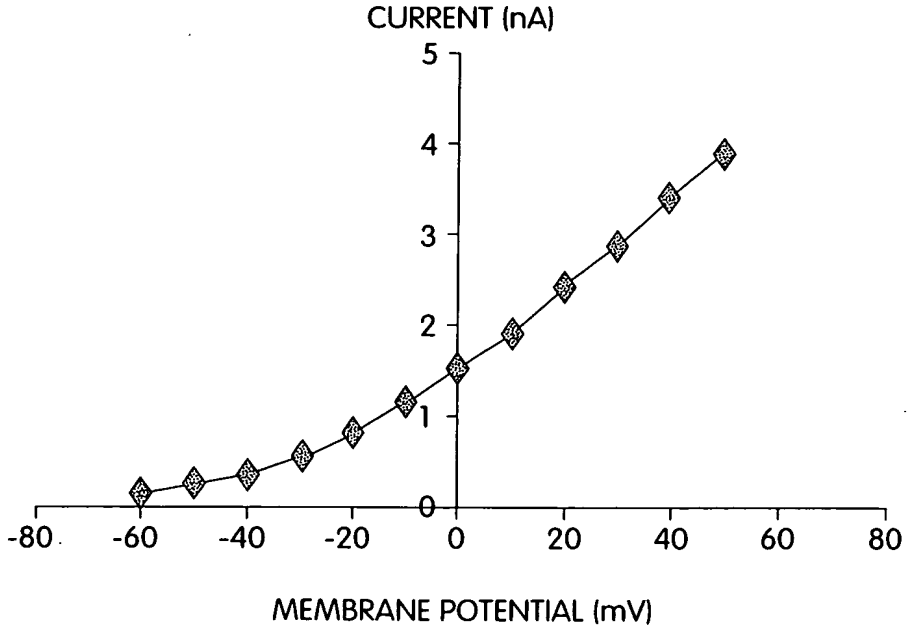

Fig. 21B

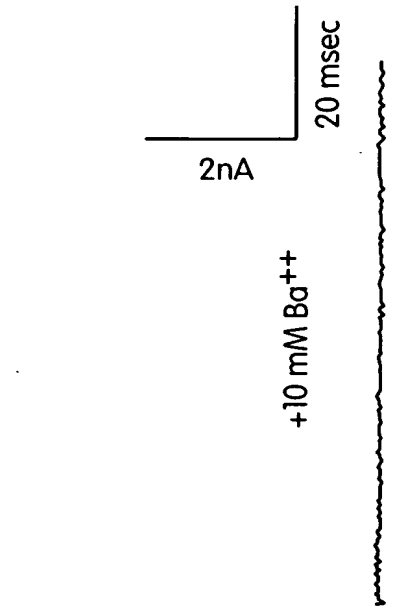

Fig. 22B

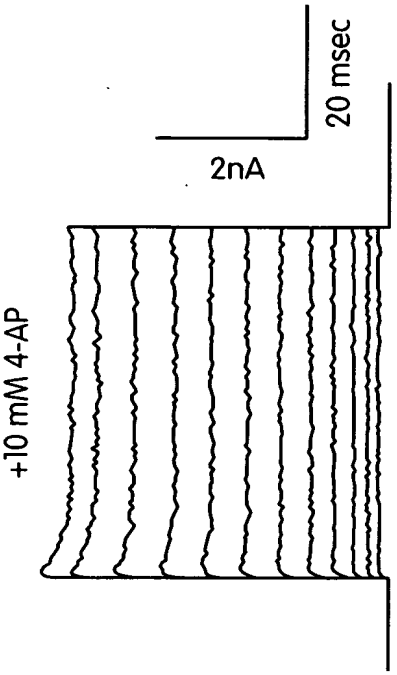

Fig. 22D

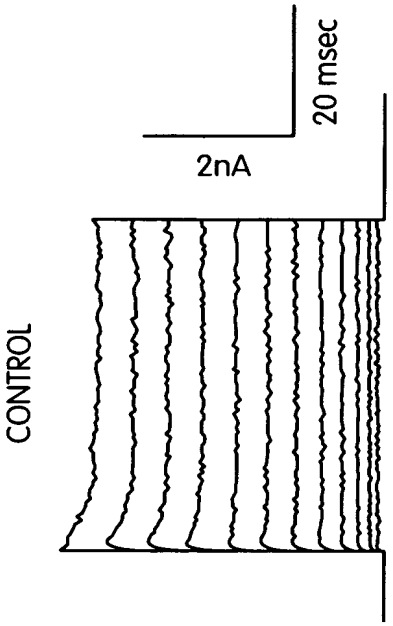

Fig. 22A

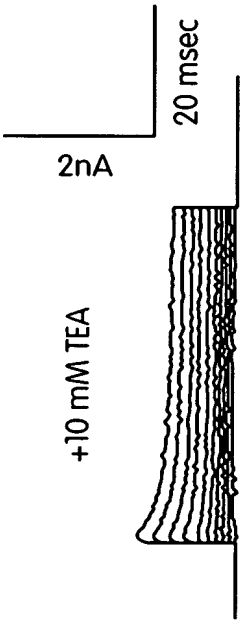

Fig. 22C